Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-9 (Canceled):

Claim 10 (Withdrawn): A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

Claim 11 (Withdrawn): A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and

(b) measuring an activity of said target.

Claim 12 (Currently amended): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is a gene product whose activity or amount is reduced by an antisense nucleic acid comprising a

nucleotide sequence selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283, provided that cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claims 13-17 (Canceled):

Claim 18 (Withdrawn): A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

Claim 19 (Withdrawn): A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

Claim 20 (Withdrawn): A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

Claims 21-28 (Canceled):

Claim 29 (Withdrawn): A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose

activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795; and

determining whether said candidate compound influences the activity of said gene product.

Claim 30 (Withdrawn): A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

Claim 31 (Currently amended): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 521, 1390, 1463, 1845, 2782 and 3283 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283; provided that said cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a nonsensitized cell.

Claims 32-36 (Canceled):

Claim 37 (Withdrawn): A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditionst;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

Claim 38 (Canceled):

Claim 39 (Withdrawn): A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said cell with a compound; and

(c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

Claims 40-44 (Canceled):

Claim 45 (Previously presented): The method of Claim 31, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 46 (Previously presented): The method of Claim 31, wherein said gene product is from an organism other than *E. coli*.

Claim 47 (Previously presented): The method of Claim 31, wherein said cell is an organism other than *E. coli*.

Claim 48 (Previously presented): The method of Claim 31, wherein said sensitized cell is a pathogenic microorganism.

Claim 49 (Previously presented): The method of Claim 31, wherein said sensitized cell is a Gram positive bacterium.

Claim 50 (Previously presented): The method of Claim 49, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 51 (Previously presented): The method of Claim 50, wherein said bacterium is *Staphylococcus aureus*.

Claim 52 (Previously presented): The method of Claim 50, wherein said *Staphylococcus* species is coagulase negative.

Claim 53 (Previously presented): The method of Claim 51, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 54 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 55 (Previously presented): The method of Claim 31, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 56 (Previously presented): The method of Claim 31, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 57 (Previously presented): The method of Claim 31, wherein said gene product is a polypeptide.

Claim 58 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 99% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 59 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 95% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 60 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 90% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 61 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 85% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide

selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 62 (Currently amended): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least ~~at least~~ 80% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 63 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 70% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 64 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 60% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 65 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 50% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from

the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 66 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 40% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 67 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 68 (Currently amended): The method of Claim 57, wherein said polypeptide is selected from the group consisting of SEQ ID NOs: 5021, 5283, 10251, 10689, 10969, 11370, 11955, 12600, 13518 and 13703.

Claim 69 (Previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 34% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 39% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 42%

amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600 and a polypeptide having at least 43% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600.

Claim 70 (Withdrawn): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 32% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 33% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 37% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689, a polypeptide having at least 63% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689 and a polypeptide having at least 77% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 10689.

Claim 71 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 97% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 72 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 95% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group

consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 73 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 90% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 74 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 85% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 75 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 80% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 76 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605 under moderate conditions.

Claim 77 (Currently amended): The method of Claim 31, wherein said nucleic acid encoding said gene product is selected from the group consisting of SEQ ID NOs: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605.

Claim 78 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 97% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 79 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 95% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 80 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 90% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 81 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 85% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 82 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 80% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 83 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 521, 1390, 1463, 1845, 2782 and 3283.

Claim 84 (Previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence comprising at least 100 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283.

Claim 85 (Previously presented): The method of Claim 12, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 86 (Currently amended): The method of Claim 12, wherein said prokaryotic organism ~~gene product is from an organism other than *E. coli*~~ is either *Staphylococcus aureus* or *Enteroccus faecalis*.

Claim 87 (Currently amended): The method of Claim ~~12~~ 86, wherein said prokaryotic organism is *Staphylococcus aureus* and said nucleotide sequence is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283 ~~cell is an organism other than *E. coli*~~.

Claim 88 (Currently amended): The method of Claim ~~12~~ 86, wherein said prokaryotic organism is *Enteroccus faecalis* and said nucleotide sequence is SEQ ID NO: 521 ~~sensitized cell is a pathogenic microorganism~~.

Claim 89 (Previously presented): The method of Claim 12, wherein said sensitized cell is a Gram positive bacterium.

Claim 90 (Previously presented): The method of Claim 89, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 91 (Previously presented): The method of Claim 90, wherein said bacterium is *Staphylococcus aureus*.

Claim 92 (Previously presented): The method of Claim 90, wherein said *Staphylococcus* species is coagulase negative.

Claim 93 (Previously presented): The method of Claim 91, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 94 (Previously presented): The method of Claim 12, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 95 (Previously presented): The method of Claim 12, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 96 (Previously presented): The method of Claim 12, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 97 (Canceled):

Claim 98 (Currently amended): The method of Claim 12 ~~97~~, wherein said gene product is a polypeptide ~~is~~ selected from the group consisting of SEQ ID NOs: ~~5021~~, 5283~~, 10251, 10689,~~ and 10969~~, 11370, 11955, 12600, 13518 and 13703~~.

Claim 99 (Currently amended): The method of Claim 12, wherein said nucleic acid encoding said gene product is selected from the group consisting of SEQ ID NOs: ~~3966,~~ 4228~~, 6154,~~ and 6592~~, 6872, 7273, 7857, 8502, 9420 and 9605~~.

Claim 100 (Currently amended): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, wherein said antisense nucleic acid reduces the activity or amount of a gene product required for cellular proliferation, thereby producing a sensitized cell, provided that said sensitized cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claim 101 (Previously presented): The method of Claim 48, wherein said pathogenic mircoorganism is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

Claim 102 (Canceled):

Claim 103 (New): The method of Claim 100, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enteroccus faecalis*.

Claim 104 (New): The method of Claim 103, wherein said prokaryotic organism is *Staphylococcus aureus* and said antisense nucleic acid is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

Claim 105 (New): The method of Claim 103, wherein said prokaryotic organism is *Enteroccus faecalis* and said antisense nucleic acid is SEQ ID NO: 521.